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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/054,536

DATE: 01/22/2003

TIME: 15:15:43

Input Set : A:\33614.txt

Output Set: N:\CRF4\01222003\J054536.raw

4 <110> APPLICANT: Wakamiya, Nobutaka
 6 <120> TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS
 7 FOR PRODUCING THE SAME
 9 <130> FILE REFERENCE: 19036/36614
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/054,536
 C--> 12 <141> CURRENT FILING DATE: 2002-01-22
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP98/03311
 15 <151> PRIOR FILING DATE: 1998-07-23
 17 <150> PRIOR APPLICATION NUMBER: JP 10-11864
 18 <151> PRIOR FILING DATE: 1998-01-23
 20 <160> NUMBER OF SEQ ID NOS: 28
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 3605
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (66)..(809)
 33 <220> FEATURE:
 34 <221> NAME/KEY: mat_peptide
 35 <222> LOCATION: (126)..(809)
 37 <400> SEQUENCE: 1
 38 ggtaaataatg tgttcattaa ctgagattaa ccttcctga gttttctcac accaaggtga 60
 40 ggacc atg tcc ctg ttt cca tca ctc cct ctc ctt ctc ctg agt atg gtg 110
 41 Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Leu Ser Met Val
 42 -20 -15 -10
 44 gca gcg tct tac tca gaa act gtg acc tgt gag gat gcc caa aag acc 158
 45 Ala Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr
 46 -5 -1 1 5 10
 48 tgc cct gca gtg att gcc tgt agc tct cca ggc atc aac ggc ttc cca 206
 49 Cys Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro
 50 15 20 25
 52 ggc aaa gat ggg cgt gat ggc acc aag gga gaa aag ggg gaa cca ggc 254
 53 Gly Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly
 54 30 35 40
 56 caa ggg ctc aga ggc tta cag ggc ccc cct gga aag ttg ggg cct cca 302
 57 Gln Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro
 58 45 50 55
 60 gga aat cca ggg cct tct ggg tca cca gga cca aag ggc caa aaa gga 350
 61 Gly Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly
 62 60 65 70 75
 64 gac cct gga aaa agt ccg gat ggt gat agt agc ctg gct gcc tca gaa 398

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65 Asp Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu
66                               80                               85                               90
68 aga aaa gct ctg caa aca gaa atg gca cgt atc aaa aag tgg ctg acc 446
69 Arg Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr
70                               95                               100                               105
72 ttc tct ctg ggc aaa caa gtt ggg aac aag ttc ttc ctg acc aat ggt 494
73 Phe Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly
74                               110                               115                               120
76 gaa ata atg acc ttt gaa aaa gtg aag gcc ttg tgt gtc aag ttc cag 542
77 Glu Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln
78                               125                               130                               135
80 gcc tct gtg gcc acc ccc agg aat gct gca gag aat gga gcc att cag 590
81 Ala Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln
82 140                               145                               150                               155
84 aat ctc atc aag gag gaa gcc ttc ctg ggc atc act gat gag aag aca 638
85 Asn Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr
86                               160                               165                               170
88 gaa ggg cag ttt gtg gat ctg aca gga aat aga ctg acc tac aca aac 686
89 Glu Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn
90                               175                               180                               185
92 tgg aac gag ggt gaa ccc aac aat gct ggt tct gat gaa gat tgt gta 734
93 Trp Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val
94                               190                               195                               200
96 ttg cta ctg aaa aat ggc cag tgg aat gac gtc ccc tgc tcc acc tcc 782
97 Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser
98                               205                               210                               215
100 cat ctg gcc gtc tgt gag ttc cct atc tgaagggtca taccactcag 829
101 His Leu Ala Val Cys Glu Phe Pro Ile
102 220                               225
104 gccctccttg tctttttact gcaaccacaca ggcccacagt atgcttgaaa agataaatta 889
106 tatcaatttc ctcatatcca gtattgttcc ttttgtgggc aatcactaaa aatgatcact 949
108 aacagcacca acaagcaat aatagtagta gtagtagtta gcagcagcag tagtagtcat 1009
110 gctaattata taatatTTTT aatatatact atgaggccct atcttttgca tcctacatta 1069
112 attatctagt ttaattaatc tgtaatgctt tcgatagtgt taacttgctg cagtatgaaa 1129
114 ataagacgga tttatttttc catttacaac aaacacctgt gctctgttga gccttccttt 1189
116 ctgtttgggt agagggtcc cctaatagaca tcaccacagt ttaataccac agctttttac 1249
118 caagtttcag gtattaagaa aatctatTTT gtaactttct ctatgaactc tgTTTTcttt 1309
120 ctaatgagat attaaacat gtaaagaaca taaataacaa atctcaagca aacagcttca 1369
122 caaattctca cacacataca tacctatata ctcaactttct agattaagat atgggacatt 1429
124 tttgactccc tagaagcccc gttataactc ctccctagtag taactcctag gaaaatacta 1489
126 ttctgacctc catgactgca cagtaatttc gtctgtttat aaacattgta tagttggaat 1549
128 catattgtgt gtaatgttgt atgtcttgct tactcagaat taagtctgtg agattcattc 1609
130 atgtcatgtg tacaaaagtt tcatcctttt cattgccatg taggggtccc ttatatatt 1669
132 attcctcagt tcatccattc tattgtttaat aggcaactaa gtggcttcca atttttggcc 1729
134 atgaggaaga gaaccacga acattcctgg acttgtcttt tgggtggacat ggtgcactaa 1789
136 tttcactacc tatccaggag tggaactggt agaggatgag gaaagcatgt attcagcttt 1849
138 agtagatatt accagttttc ctaagtgatt gtatgaattt atgctcctac cggcaatgtg 1909
140 tggcagtcct agatgctcta tgtgcttgta aaaagtcaat gttttcagtt ctcttgattt 1969
142 tcattattcc tgtggatgta aagtgatatt tccccatggt tttaatctgt atttcccaaa 2029

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144 catgtaataa ggttgaacac ttttttatat gcttattggg cacttgggta tcttcttctg 2089
146 tgaagtaccc gttcacattt ttgtattttg tttaaattag ttagccaata tttttcttac 2149
148 tgatttttaa gttattttta cattctgaat atgtcctttt taatgtgtat tacaaatatt 2209
150 ttgctagttt ttgacttgct cctaagtgtg aattttgatg aacaaaattt cctaattttg 2269
152 agaaagtctt atttattcat attttctttc aaaattagtg ctttttgtgt catgtttaag 2329
154 aaatttttgc ccatcccaaa atcataagat atttttcatg attttgaaac catgaagaga 2389
156 tttttcatga ttttgaaatc atgaagatat ttttccattt ttttctaata gttttattaa 2449
158 taaacattct atctattcct ggtagaatag atatccactt gagacagcac tatgtaggaa 2509
160 agaccatttt tcctccactg aactagggtg gtgcattttt gtaagttagg taactgtatg 2569
162 tgtgtgtgtc tgtttctggg ctgtctattc tagtctattt gttgatgctt gtgtcaaaca 2629
164 gtacactatc ttaattattg tacatttata gttgtaactg tagtccagct ttgttcttct 2689
166 tcaagtcaag atttccatat aaatattaga aacagtttct caatttctac aaaatcctga 2749
168 tgaggtttct actgggacca cattgagtct atcaatcaac ttatgcagaa ctggcaactt 2809
170 actactgaat ctctaataaa tgttcatcat gtatcgcttc atttaactag gatttctcta 2869
172 acttaattgc tatgttttga gatttttagt ttaaaaacct tgtatatctt gttttggtgg 2929
174 ttttagtgat tttaataata tatttttaaat atttttctt ttctattgtt gtacacagaa 2989
176 atacagttaa gttttgtgtg tagtcttacg atgttttagta acctcaataa gtttatttct 3049
178 taaatctagt aatttgtaga ttctcttgga ttttgtatat gcatagtcat gtaagctgaa 3109
180 aatatggcaa tacttgcttc ttcccaattg ctttaccttt tttcttacct tattgcactg 3169
182 gttagcaacc ccaatacaga gaccaccaga gcaggatag actcctgaaa gacaatataa 3229
184 tgaagtgtc cagtcaggcc tatctaaact ggattcacag ctctgtcact taattgctac 3289
186 atgatctaga gccagttact ttgtgtttca gccatgtatt tgcagctgag agaaaataat 3349
188 cattcttatt tcatgaaaat tgtggggatg atgaaataag ttaacacctt taaagtgtgt 3409
190 agtaaagtat caggatacta tatttttaggt cttaatacac acagttatgc cgctagatac 3469
192 atgcttttta atgagataat gtgatattat acataacaca tatcgatttt taaaaattaa 3529
194 atcaaccttg ctttgatgga ataaactcca tttagtcaca aaaaaaaaaa aaaaaaaaaa 3589
196 aaaaaaaaaa aaaaaa 3605

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199 <210> SEQ ID NO: 2

200 <211> LENGTH: 747

201 <212> TYPE: DNA

202 <213> ORGANISM: Homo sapiens

204 <400> SEQUENCE: 2

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205 atgtccctgt ttccatcact ccctctcctt ctcttgagta tgggtggcagc gtcttactca 60
207 gaaactgtga cctgtgagga tgcccaaaag acctgccctg cagtgattgc ctgtagctct 120
209 ccaggcatca acggcttccc aggcaaagat gggcgtgatg gcaccaaggg agaaaagggg 180
211 gaaccaggcc aagggtcag aggcttacag ggccccctg gaaagtggg gcctccagga 240
213 aatccagggc cttctgggtc accaggacca aagggccaaa aaggagacc tggaaaaagt 300
215 ccggatggtg atagtagcct ggctgcctca gaaagaaaag ctctgcaaac agaaatggca 360
217 cgtatcaaaa agtggctgac cttctctctg ggcaacaag ttgggaacaa gttcttctg 420
219 accaatggtg aaataatgac ctttgaaaaa gtgaaggcct tgtgtgtcaa gttccaggcc 480
221 tctgtggcca ccccaggaa tgctgcagag aatggagcca ttcagaatct catcaaggag 540
223 gaagccttcc tgggcatcac tgatgagaag acagaagggc agtttgtgga tctgacagga 600
225 aatagactga cctacacaaa ctggaacgag ggtgaacca acaatgctgg ttctgatgaa 660
227 gattgtgtat tgctactgaa aaatggccag tggaatgacg tcccctgctc cacctcccat 720
229 ctggccgtct gtgagttccc tatctga 747

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232 <210> SEQ ID NO: 3

233 <211> LENGTH: 41

234 <212> TYPE: DNA

235 <213> ORGANISM: Artificial Sequence

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237 <220> FEATURE:
 238 <223> OTHER INFORMATION: Description of Artificial Sequence: sense DNA
 240 <400> SEQUENCE: 3
 241 tatgccgcgg aatcgatgat taccgtacgg aattcgggcc c 41
 244 <210> SEQ ID NO: 4
 245 <211> LENGTH: 39
 246 <212> TYPE: DNA
 247 <213> ORGANISM: Artificial Sequence
 249 <220> FEATURE:
 250 <223> OTHER INFORMATION: Description of Artificial Sequence: antisense DNA
 252 <400> SEQUENCE: 4
 253 acggcgcctt agctactaat ggcattgcctt aagcccggg 39
 256 <210> SEQ ID NO: 5
 257 <211> LENGTH: 29
 258 <212> TYPE: DNA
 259 <213> ORGANISM: Artificial Sequence
 261 <220> FEATURE:
 262 <223> OTHER INFORMATION: Description of Artificial Sequence: sense DNA
 264 <400> SEQUENCE: 5
 265 agcttccgcg gctgcaggga tccatcgat 29
 268 <210> SEQ ID NO: 6
 269 <211> LENGTH: 29
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Artificial Sequence
 273 <220> FEATURE:
 274 <223> OTHER INFORMATION: Description of Artificial Sequence: antisense DNA
 276 <400> SEQUENCE: 6
 277 aggcgcgcgac gtccctaggt agctattaa 29
 280 <210> SEQ ID NO: 7
 281 <211> LENGTH: 37
 282 <212> TYPE: DNA
 283 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 286 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' sense
 287 primer (PS1)
 289 <400> SEQUENCE: 7
 290 cccgcgcggga attctgtgga atgtgtgtca gttaggg 37
 293 <210> SEQ ID NO: 8
 294 <211> LENGTH: 32
 295 <212> TYPE: DNA
 296 <213> ORGANISM: Artificial Sequence
 298 <220> FEATURE:
 299 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' antisense
 300 primer (PS2)
 302 <400> SEQUENCE: 8
 303 ccctgcagct ttttgcaaaa gcctaggcct cc 32
 306 <210> SEQ ID NO: 9
 307 <211> LENGTH: 31
 308 <212> TYPE: DNA

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309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' sense
313     primer (PS3)
315 <400> SEQUENCE: 9
316 ccccgcggtg tggaaatgtgt gtcagttagg g                      31
319 <210> SEQ ID NO: 10
320 <211> LENGTH: 16
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Description of Artificial Sequence: sense DNA
327 <400> SEQUENCE: 10
328 aattgggccc atcgat                      16
331 <210> SEQ ID NO: 11
332 <211> LENGTH: 16
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence: antisense DNA
339 <400> SEQUENCE: 11
340 cccgggtagc tattaa                      16
343 <210> SEQ ID NO: 12
344 <211> LENGTH: 41
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' sense
350     primer (PD1)
352 <400> SEQUENCE: 12
353 ggctgcagtc cctcatgctt cgaccattga actgcacgt c              41
356 <210> SEQ ID NO: 13
357 <211> LENGTH: 32
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial Sequence
361 <220> FEATURE:
362 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' antisense
363     primer (PD2)
365 <400> SEQUENCE: 13
366 atagatctaa agccagcaaa agtcccatgg tc                      32
369 <210> SEQ ID NO: 14
370 <211> LENGTH: 28
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' sense
376     primer (PN1)
378 <400> SEQUENCE: 14
379 ggctgcagct tcacgctgcc gcaagcac                      28

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/054,536

DATE: 01/22/2003

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Input Set : A:\33614.txt

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date